

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 13:13:15 ; Search time 30.02 seconds
(without alignments)
340.399 Million cell updates/sec

Title: US-09-218-913D-8

Perfect score: 501

Sequence: 1 ADNRSTHDFCLSVKVVGR.....ATSRNAADSSVPSAPRRQDS 92

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

- 1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
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- 10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
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- 12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
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- 14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
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- 19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	100.0	92	18 AAW30054	Human placental bi
2	501	100.0	92	21 AAB14166	Human placental bi
3	501	100.0	170	18 AAW30041	Human placental bi
4	501	100.0	170	21 AAB14189	Human placental bi
5	501	100.0	170	21 AAB14190	Human placental bi
6	501	100.0	179	18 AAW30053	Human placental bi
7	501	100.0	179	21 AAB14159	Mature human place
8	501	100.0	197	18 AAW30043	Human placental bi
9	501	100.0	197	21 AAB14160	Human placental bi
10	501	100.0	213	18 AAW30042	Human placental bi
11	501	100.0	213	21 AAB14184	Human placental bi

12	501	100.0	213	21 AAB14200	Human placental bi
13	501	100.0	225	18 AAW30046	Human placental bi
14	501	100.0	225	21 AAB14186	Human placental bi
15	501	100.0	225	21 AAB14201	Human placental bi
16	501	100.0	235	18 AAW30060	Human consensus bi
17	501	100.0	235	21 AAB14167	Human placental bi
18	501	100.0	240	18 AAW30045	Human placental bi
19	501	100.0	240	21 AAB14185	Human placental bi
20	501	100.0	248	18 AAW30044	Human consensus bi
21	501	100.0	248	21 AAB14183	Human placental bi
22	501	100.0	252	18 AAW30040	Human placental bi
23	501	100.0	252	18 AAW13665	Hepatocyte growth
24	501	100.0	252	19 AAW70286	Human tissue facto
25	501	100.0	252	21 AAB14187	Human placental bi
26	501	100.0	259	21 AAB14207	Human placental bi
27	501	100.0	289	21 ABA43821	Human cancer assoc
28	498	99.4	252	21 ABB50286	Kunitz type 2 Ser
29	490	97.8	130	21 AAB14169	Human placental bi
30	488	97.4	130	18 AAW30062	EST R35464 protein
31	472	94.2	153	18 AAW30051	Human placental bi
32	472	94.2	153	21 AAB14161	Human placental bi
33	448	89.4	146	18 AAW30052	Human placental bi
34	448	89.4	146	21 AAB14188	Human placental bi
35	403	80.4	170	18 AAW30061	Human consensus bi
36	403	80.4	179	21 AAB14168	Human placental bi
37	334	66.7	58	18 AAW30047	Human placental bi
38	334	66.7	58	21 AAB14162	Human placental bi
39	297	59.3	51	18 AAW30048	Human placental bi
40	297	59.3	51	21 AAB14163	Human placental bi
41	203	40.5	529	22 AAE09332	Human PRO256 prote
42	203	40.5	529	22 AAB20113	Human immunostimul
43	197	39.3	513	18 AAW27368	Hepatocyte growth
44	197	39.3	513	20 AAW26553	Human HAI-1 protei
45	197	39.3	513	21 AAB19553	Human hepatocyte g

ALIGNMENTS

RESULT 1
AAW30054
ID AAW30054 standard; Protein; 92 AA.
XX AC AAW30054;
XX DT 20-APR-1998 (first entry)
XX DE Human placental bikunin.
XX KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX OS Homo sapiens.
XX PN WO9733996-A2.
XX PD 18-SEP-1997.
XX PF 10-MAR-1997; 97WO-US03894.
XX PR 04-OCT-1996; 96US-0725251.
XX PR 11-MAR-1996; 96US-0013106.
XX PR 14-JUN-1996; 96US-0019793.
XX PA (FARB) BAYER CORP.
XX PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX WPI; 1997-470876/43.

XX New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 67; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 501; DB 18; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADRERSTHDFCLVSKVVGRCRASMPrwYnVTDGSCQLFVYGCDGNSNNYLTKECLKK 60
|||||
Db 1 adersihdfclvskvvgrcrasmprrwYnVTDGSCQLFVYGCDGNSNNYLTKECLKK 60
|||||

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
|||||
Db 61 catvtenatgdlatsrnaadssvpsaprrqds 92
|||||

RESULT 2
AAB14166
ID AAB14166 standard; protein; 92 AA.
AC AAB14166;
XX
XX 02-FEB-2001 (first entry)
XX Human placental bikunin protein fragment # 6.
XX
DE Human; mucociliary dysfunction; mucus; sputum;
DE chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
XX
XX Homo sapiens.
XX
PN WO200037099-A2.
XX
XX 29-JUN-2000.
XX
XX 22-DEC-1999; 99WO-GB04381.
XX
XX 22-DEC-1998; 98US-0218913.
PR 17-NOV-1999; 99US-0441966.
XX
XX (FARB) BAYER AG.
XX
XX Hall R, Poll CT, Newton BB, Taylor WJA;
XX

DR WPI; 2000-452127/39.
XX Stimulating mucociliary clearance rate of mucus and sputum in lung
PT airways for treating lung diseases such as cystic fibrosis and
PT bronchitis involves administering a Kunitz-type serine protease
PT inhibitor -
XX
PS Claim 15; Page 90; 173pp; English.
XX
CC Mucociliary dysfunction is the inability of ciliated epithelium to clear
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
CC complication of chronic obstructive lung diseases such as Chronic
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
CC In addition, patients suffering from mucociliary dysfunction are
CC susceptible to secondary bacterial infections. The present sequence is a
CC fragment of human placental bikunin. Human placental bikunin is a
CC Kunitz-type serine protease inhibitor protein, which can stimulate the
CC rate of mucociliary clearance of mucus and sputum in lung airways.
CC Therefore, the present protein fragment may be used for treating lung
CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which
CC are caused by retention and accumulation of mucus. The present sequence
CC consists of residues 1-92 of the mature human placental bikunin
CC protein sequence, which is described in AAB14159.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 501; DB 21; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADRERSTHDFCLVSKVVGRCRASMPrwYnVTDGSCQLFVYGCDGNSNNYLTKECLKK 60
|||||
Db 1 adersihdfclvskvvgrcrasmprrwYnVTDGSCQLFVYGCDGNSNNYLTKECLKK 60
|||||

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
|||||
Db 61 catvtenatgdlatsrnaadssvpsaprrqds 92
|||||

RESULT 3
AAB30041
ID AAB30041 standard; Protein; 170 AA.
XX
XX AAB30041;
XX
XX 20-APR-1998 (first entry)
XX Human placental bikunin.
XX
DE Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
XX Homo sapiens.
XX
PN WO9733996-A2.
XX
XX 18-SEP-1997.
XX
XX 10-MAR-1997; 97WO-US03894.
XX
XX 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
XX (FARB) BAYER CORP.
XX
XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX

PI Hall R, Poll CT, Newton BB, Taylor WJA;

PI Hall R, Poll CT, Newton BB, Taylor WJA;

XX WPI; 2000-452127/39.
 DR Stimulating mucociliary clearance rate of mucus and sputum in lung
 XX PT airways for treating lung diseases such as cystic fibrosis and
 PT bronchitis involves administering a Kunitz-type serine protease
 XX inhibitor
 XX
 PS Claim 14; Pages 89-90; 173pp; English.
 XX
 CC The present sequence is the inability of ciliated epithelium to clear
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
 CC complication of chronic obstructive lung diseases such as Chronic
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
 CC In addition, patients suffering from mucociliary dysfunction are
 CC susceptible to secondary bacterial infections. The present sequence is
 CC human placental bikunin. This protein is a Kunitz-type serine protease
 CC inhibitor protein, which can stimulate the rate of mucociliary clearance
 CC of mucus and sputum in lung airways. Therefore, the present protein may
 CC be used for treating lung diseases such as CF, CB, BE, and chronic
 CC sinusitis and glue ear which are caused by retention and accumulation of
 CC mucus. The present sequence is the mature human placental bikunin protein
 CC sequence.
 XX
 SQ Sequence 179 AA;
 Query Match 100.0%; Score 501; DB 21; Length 179;
 Best Local Similarity 100.0%; Pred. No. 2.4e-50;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADERSIHDFCLVSKVVGRCRASPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 60
 Db 1 adersihdfclvskvvgrcrasprwvnyntdgsqclfvyyggdgnnsnyltkeecclk 60
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
 Db 61 catvtenatgdlatsrnaadssvpsaprrqds 92
 RESULT 8
 AAW30043
 ID AAW30043 standard; Protein; 197 AA.
 XX
 AC AAW30043;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE Human placental bikunin.
 XX
 KW Human; placental bikunin; inhibition; trypsin; kallikrein;
 KW plasmin; factor xiiia; treatment; prevention; oedema;
 KW inflammation; infection; granulomatosis; multiple sclerosis;
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;
 KW gastric cancer; cervical cancer; metastasis; blood loss.
 XX
 OS Homo sapiens.
 XX
 PN WO9733996-A2.
 XX
 PD 18-SEP-1997.
 XX
 PF 10-MAR-1997; 97WO-US03894.
 XX
 PR 04-OCT-1996; 96US-0725251.
 XX
 PR 11-MAR-1996; 96US-0013106.
 XX
 PR 14-JUN-1996; 96US-0019793.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
 XX

DR WPI; 1997-470876/43.
 XX
 PT New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss
 XX
 PS Claim 1; Page 65; 110pp; English.
 XX
 CC The present sequence is a human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC aprotinin, but is less highly charged so should be less
 CC immunogenic and less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.
 XX
 SQ Sequence 197 AA;
 Query Match 100.0%; Score 501; DB 18; Length 197;
 Best Local Similarity 100.0%; Pred. No. 2.7e-50;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 19 adersihdfclvskvvgrcrasprwvnyntdgsqclfvyyggdgnnsnyltkeecclk 78
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
 Db 79 catvtenatgdlatsrnaadssvpsaprrqds 110
 RESULT 9
 AAB14160
 ID AAB14160 standard; protein; 197 AA.
 XX
 AC AAB14160;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Human placental bikunin mature protein and signal peptide.
 XX
 KW Human; mucociliary dysfunction; mucus; sputum;
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
 XX
 OS Homo sapiens.
 XX
 PN WO200037099-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 22-DEC-1999; 99WO-GB04381.
 XX

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PR 22-DEC-1998; 98US-0218913.
XX 17-NOV-1999; 99US-0441966.
PA (FARB ) BAYER AG.
XX
PI Hall R, Poll CT, Newton BB, Taylor WJA;
XX
DR WPI; 2000-452127/39.
XX
XX Stimulating mucociliary clearance rate of mucus and sputum in lung
PT airways for treating lung diseases such as cystic fibrosis and
PT bronchitis involves administering a Kunitz-type serine protease
PT inhibitor -
XX
XX Claim 13; Page 88; 173pp; English.
PS
XX Mucociliary dysfunction is the inability of ciliated epithelium to clear
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
CC complication of chronic obstructive lung diseases such as Chronic
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
CC In addition, patients suffering from mucociliary dysfunction are
CC susceptible to secondary bacterial infections. The present sequence is
CC human placental bikunin. This protein is a Kunitz-type serine protease
CC inhibitor protein, which can stimulate the rate of mucociliary clearance
CC of mucus and sputum in lung airways. Therefore, the present protein may
CC be used for treating lung diseases such as CF, CB, BE, and chronic
CC sinusitis and glue ear which are caused by retention and accumulation of
CC mucus. The present sequence is the full-length human placental bikunin
CC protein sequence.
XX
XX Sequence 197 AA;
SQ
Query Match 100.0%; Score 501; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.7e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADRESIHDFCLVSKVVGRCRSMRWYNYVTDGSCQLFVYGGCDGNSNNYITKEECLKK 60
DB 19 adreSIHdfclvskvvgvgrcrasmrwyNvtdgscqlfvyggcdgnsnnYitkeeclkk 78
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
DB 79 catvtENatgdlatsrNaadssvpsaprrqds 110
RESULT 10
AAW30042
ID AAW30042 standard; Protein; 213 AA.
XX
AC AAW30042;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.

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PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB ) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
DR WPI; 1997-470876/43.
XX
XX New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
XX Claim 1; Page 65; 110pp; English.
PS
XX The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
XX Sequence 213 AA;
SQ
Query Match 100.0%; Score 501; DB 18; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADRESIHDFCLVSKVVGRCRSMRWYNYVTDGSCQLFVYGGCDGNSNNYITKEECLKK 60
DB 1 adreSIHdfclvskvvgvgrcrasmrwyNvtdgscqlfvyggcdgnsnnYitkeeclkk 60
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
DB 61 catvtENatgdlatsrNaadssvpsaprrqds 92
RESULT 11
AAB14184
ID AAB14184 standard; protein; 213 AA.
XX
AC AAB14184;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human placental bikunin protein # 2.
XX
KW Human; mucociliary dysfunction; mucus; sputum;
KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
XX
OS Homo sapiens.
XX
PN WO200037099-A2.
XX
PD 29-JUN-2000.
XX
PF 22-DEC-1999; 99WO-GB04381.
XX

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Stimulating mucociliary clearance rate of mucus and sputum in lung airways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease inhibitor -

Claim 13; Page 88; 173pp; English.

Mucociliary dysfunction is the inability of ciliated epithelium to clear mucus and sputum in lung airways. Mucociliary dysfunction is a serious complication of chronic obstructive lung diseases such as Chronic Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF). In addition, patients suffering from mucociliary dysfunction are susceptible to secondary bacterial infections. The present sequence is a fragment of human placental bikunin. Human placental bikunin is a Kunitz-type serine protease inhibitor protein, which can stimulate the rate of mucociliary clearance of mucus and sputum in lung airways. Therefore, the present protein fragment may be used for treating lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are caused by retention and accumulation of mucus.

Local Similarity

Query Match	100.0%;	Score 501;	DB 21;	Length 213;
Best Local Similarity	100.0%;	Pred. No. 2.9e-50;		
Matches 92;	Conservative 0;	Mismatches 0;	Indels 0;	

[illegible]

61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 922
|||||
61 catvtenatgdlatsrnaadssvpsaprrqds 922

RESULT 12

AAW30040
ID AAW30046 standard; protein; 225 AA.

AAW30046;

20-APR-1998 (first entry)

Human placental bikunin.

Human; placental bikunin; inhibition; trypsin; kallikrein; plasmin; factor XIII; treatment; prevention; oedema; inflammation; infection; granulomatosis; multiple sclerosis; ischaemia; perioperative blood loss; sepsis; shock; fibrosis; blood coagulation disease; polytrauma; stroke; haemorrhage; gastric cancer; cervical cancer; metastasis; blood loss.

Homo sapiens.

PN WO9733996-A2.

PD 18-SEP-1997.

10-MAR-1997: 97WO-US03894.

PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106

PR II-MAR-1996; 96US-0013106.
PR 14-JUN-1996. 96US-0019793

PA (FARB) BAYER CORP.
 PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
 XX
 XX WPI; 1997-470876/43.
 XX
 XX New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss
 XX
 XX Claim 1; Page 66; 110pp; English.
 PS
 XX The present sequence is a human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC aprotinin, but is less highly charged so should be less
 CC immunogenic and less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.
 XX
 XX Sequence 225 AA;
 SQ

Query Match 100.0%; Score 501; DB 18; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.1e-50;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRASMPrwYnVTDGSCQLFVYGCDGNSNNYLTKECLKK 60
 |||||||
 Db 1 adersiHdfclvskvvgrcrasmprwYnvtDgscqlfvyggcdgnsnnYltkeecLkK 60
 |||||||

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
 |||||||
 Db 61 catvtEnatgdlatsrnaadssvpsaprrqds 92
 |||||||

RESULT 14
 AAB14186
 ID AAB14186 standard; protein; 225 AA.
 XX
 AC AAB14186;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Human placental bikunin protein # 4.
 XX
 KW Human; mucociliary dysfunction; mucus; sputum;
 KW Chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
 XX
 OS Homo sapiens.
 XX
 PN WO200037099-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 22-DEC-1999; 99WO-GB04381.
 XX
 PR 22-DEC-1998; 98US-0218913.
 PR 17-NOV-1999; 99US-0441966.

(FARB) BAYER AG.
 Hall R, Poll CT, Newton BB, Taylor WJA;
 WPI; 2000-452127/39.
 Stimulating mucociliary clearance rate of mucus and sputum in lung
 airways for treating lung diseases such as cystic fibrosis and
 bronchitis involves administering a Kunitz-type serine protease
 inhibitor -
 Disclosure; Page 164; 173pp; English.
 Mucociliary dysfunction is the inability of ciliated epithelium to clear
 mucus and sputum in lung airways. Mucociliary dysfunction is a serious
 complication of chronic obstructive lung diseases such as Chronic
 Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
 In addition, patients suffering from mucociliary dysfunction are
 susceptible to secondary bacterial infections. The present sequence is a
 fragment of human placental bikunin. Human placental bikunin is a
 Kunitz-type serine protease inhibitor protein, which can stimulate the
 rate of mucociliary clearance of mucus and sputum in lung airways.
 Therefore, the present protein fragment may be used for treating lung
 diseases such as CF, CB, BE, and chronic sinusitis and glue ear which
 are caused by retention and accumulation of mucus.
 Note: the present sequence is defined as SEQ ID 48 in the sequence
 listing. However, in figure 4F of the specification, SEQ ID 48 is
 clearly shown as a nucleotide sequence. Therefore, the nucleotide
 sequence has been described in AAA70406.
 XX
 SQ Sequence 225 AA;
 Query Match 100.0%; Score 501; DB 21; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.1e-50;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRASMPrwYnVTDGSCQLFVYGCDGNSNNYLTKECLKK 60
 |||||||
 Db 1 adersiHdfclvskvvgrcrasmprwYnvtDgscqlfvyggcdgnsnnYltkeecLkK 60
 |||||||

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
 |||||||
 Db 61 catvtEnatgdlatsrnaadssvpsaprrqds 92
 |||||||

RESULT 15
 AAB14201
 ID AAB14201 standard; protein; 225 AA.
 XX
 AC AAB14201;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Human placental bikunin protein fragment # 16.
 XX
 KW Human; mucociliary dysfunction; mucus; sputum;
 KW Chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
 XX
 OS Homo sapiens.
 XX
 PN WO200037099-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 22-DEC-1999; 99WO-GB04381.
 XX
 PR 22-DEC-1998; 98US-0218913.
 PR 17-NOV-1999; 99US-0441966.

PA (FARB) BAYER AG.
XX
PI Hall R, Poll CT, Newton BB, Taylor WJA;
XX
DR WPI; 2000-452127/39.
XX
PT Stimulating mucociliary clearance rate of mucus and sputum in lung
PT airways for treating lung diseases such as cystic fibrosis and
PT bronchitis involves administering a Kunitz-type serine protease
PT inhibitor
XX
PS Claim 13; Pages 88-89; 173pp; English.
XX
CC Mucociliary dysfunction is the inability of ciliated epithelium to clear
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
CC complication of chronic obstructive lung diseases such as Chronic
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
CC In addition, patients suffering from mucociliary dysfunction are
CC susceptible to secondary bacterial infections. The present sequence is a
CC fragment of human placental bikunin. Human placental bikunin is a
CC Kunitz-type serine protease inhibitor protein, which can stimulate the
CC rate of mucociliary clearance of mucus and sputum in lung airways.
CC Therefore, the present protein fragment may be used for treating lung
CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are
CC caused by retention and accumulation of mucus.
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 501; DB 21; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.1e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGCRASMPRWYNYVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 adersihdfclvskvvgcrasmprwynvtdgscqlfvyggcdgnsnnytkeecikk 60

QY 61 CATVTENATGDIATSRNAADSSVPSAPRRQDS 92
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 catvtenatgdiatsrnaadssvpsaprrqds 92

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OM protein - protein search, using sw model

Run on: September 10, 2002, 13:15:15 ; Search time 13.01 Seconds
(without alignments)
172.725 Million cell updates/sec

Title: US-09-218-913D-8

Perfect score: 501

Sequence: 1 ADERSIHDFCLVSKVVGRC.....ATSRNAADSVPSAPRRQDS 92

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	100.0	252	1	US-08-685-660A-7
2	501	100.0	252	2	US-08-974-196-7
3	501	100.0	252	4	US-09-071-709-10
4	501	100.0	252	4	US-09-013-896A-2
5	297	59.3	51	4	US-09-013-896A-10
6	197	39.3	51	4	US-08-685-558A-18
7	192.5	38.4	348	4	US-09-071-709-2
8	180	35.9	58	1	US-08-358-160-71
9	174	34.7	58	3	US-08-676-124-93
10	174	34.7	58	3	US-09-414-878-93
11	174	34.7	58	3	US-09-240-136-93
12	167	33.3	62	1	US-08-358-160-97
13	166	33.1	58	3	US-08-676-124-126
14	166	33.1	58	3	US-09-414-878-126
15	166	33.1	58	3	US-09-240-136-126
16	165	32.9	51	4	US-09-013-896A-28
17	165	32.9	58	3	US-08-676-124-95
18	165	32.9	58	3	US-09-414-878-95
19	165	32.9	58	3	US-09-240-136-95
20	164	32.7	58	1	US-08-463-155A-64
21	164	32.7	58	1	US-08-463-432B-64
22	163	32.5	51	4	US-09-013-896A-11
23	163	32.5	58	1	US-07-664-989B-48
24	163	32.5	58	1	US-08-358-160-1
25	163	32.5	58	1	US-08-463-155A-57
26	163	32.5	58	1	US-08-463-432B-57
27	163	32.5	58	1	US-08-676-125A-23

28 163 32.5 58 1 US-08-676-125A-46 Sequence 46, Appl
29 163 32.5 58 2 US-09-136-012A-23 Sequence 23, Appl
30 163 32.5 58 2 US-09-136-012A-46 Sequence 46, Appl
31 163 32.5 58 3 US-08-676-124-77 Sequence 77, Appl
32 163 32.5 58 3 US-09-414-878-77 Sequence 77, Appl
33 163 32.5 58 3 US-09-240-136-77 Sequence 77, Appl
34 162 32.3 58 1 US-07-664-989B-49 Sequence 49, Appl
35 162 32.3 58 1 US-08-358-160-24 Sequence 24, Appl
36 162 32.3 58 1 US-08-358-160-26 Sequence 26, Appl
37 162 32.3 58 1 US-08-463-155A-3 Sequence 3, Appl
38 162 32.3 58 1 US-08-463-432B-3 Sequence 3, Appl
39 162 32.3 58 1 US-08-676-124-125 Sequence 125, App
40 162 32.3 58 3 US-09-414-878-125 Sequence 125, App
41 162 32.3 58 3 US-09-240-136-125 Sequence 125, App
42 162 32.3 58 3 US-08-358-160-27 Sequence 27, Appl
43 162 32.1 58 1 US-07-664-989B-87 Sequence 87, Appl
44 161 32.1 58 1 US-08-358-160-17 Sequence 17, Appl
45

ALIGNMENTS

RESULT 1
US-08-685-660A-7
; Sequence 7, Application US/08685660A
; Patent No. 5731412
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,660A
; FILING DATE: 24-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JPA Hei 7-187134
; FILING DATE: 24-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: Q-42295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-685-660A-7

Query Match 100.0% Score 501; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-52;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ADERSIHDFCLVSKVVGRCASMPWWNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60

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Db      28 ADERSIHDFCLVSKVVGRCRASMPRWYNVTDGSCQLFYGGCDGNSNNYLTKEECLKK 87
      61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
      88 CATVTENATGDLATSRNAADSSVPSAPRRQDS 119

RESULT 2
US-08-974-196-7
; Sequence 7, Application US/08974196
; Patent No. 5854396
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,196
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,660
; FILING DATE: 24-JUL-1996
; APPLICATION NUMBER: JPA Hei 7-187134
; FILING DATE: 24-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: Q-42295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-196-7
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Query Match      100.0%; Score 501; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-52;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADERSIHDFCLVSKVVGRCRASMPRWYNVTDGSCQLFYGGCDGNSNNYLTKEECLKK 60
      28 ADERSIHDFCLVSKVVGRCRASMPRWYNVTDGSCQLFYGGCDGNSNNYLTKEECLKK 87
      61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
      88 CATVTENATGDLATSRNAADSSVPSAPRRQDS 119
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RESULT 3
US-09-071-709-10
; Sequence 10, Application US/09071709
; Patent No. 6171790
; GENERAL INFORMATION:
```

```
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Lal, preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,709
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0513 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-709-10

Query Match      100.0%; Score 501; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-52;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADERSIHDFCLVSKVVGRCRASMPRWYNVTDGSCQLFYGGCDGNSNNYLTKEECLKK 60
      28 ADERSIHDFCLVSKVVGRCRASMPRWYNVTDGSCQLFYGGCDGNSNNYLTKEECLKK 87
      61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
      88 CATVTENATGDLATSRNAADSSVPSAPRRQDS 119

RESULT 4
US-09-013-896A-2
; Sequence 2, Application US/09013896A
; Patent No. 6262233
; GENERAL INFORMATION:
; APPLICANT: GENTZ, REINER
; TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, STE. 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/013.896A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STEFFE, ERIC K.
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.1290001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 252 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-013-896A-2

Query Match 100.0%; Score 501; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-52;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADRESIHDFCLVSKVVGCRASMPRWYNTDGSQFLFVYGGCDGNSNNYLTKEECLKK 60
Db 28 ADRESIHDFCLVSKVVGCRASMPRWYNTDGSQFLFVYGGCDGNSNNYLTKEECLKK 87

Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
Db 88 CATVTENATGDLATSRNAADSSVPSAPRRQDS 119

RESULT 5
US-09-013-896A-10
; Sequence 10, Application US/09013896A
; Patent No. 6262233
; GENERAL INFORMATION:
; APPLICANT: GENTZ, REINER
; TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, STE. 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013.896A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1290001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-013-896A-10

Query Match 59.3%; Score 297; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1e-28;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CLVSKVVGCRASMPRWYNTDGSQFLFVYGGCDGNSNNYLTKEECLKK 61
Db 1 CLVSKVVGCRASMPRWYNTDGSQFLFVYGGCDGNSNNYLTKEECLKK 51

RESULT 6
US-08-685-558A-18
; Sequence 18, Application US/08685558A
; Patent No. 6225081
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; APPLICANT: MIYAZAWA, Keiji
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,558A
; FILING DATE: 24-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JPA Hei 7-187135
; FILING DATE: 24-JUL-1995
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 513 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: MKN45
US-08-685-558A-18

Query Match 39.3%; Score 197; DB 4; Length 513;
Best Local Similarity 55.0%; Pred. No. 1.6e-15;
Matches 33; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 5 RSIHDFCLVSKVVGCRASMPRWYNTDGSQFLFVYGGCDGNSNNYLTKEECLKKCATV 64
Db 244 KOTEDYCLASNKVGRGSPRWYDPTQICKSFVYGGCLGNKNYDREECILACRGV 303

RESULT 7
US-09-071-709-2
; Sequence 2, Application US/09071709
; Patent No. 6171790
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra

;; TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;; STREET: 3174 PORTER DRIVE
;; CITY: PALO ALTO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/071,709
;; FILING DATE: Filed Herewith
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CERRONE, MICHAEL C.
;; REGISTRATION NUMBER: 39,132
;; REFERENCE/DOCKET NUMBER: PF-0513 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 855-0555
;; TELEFAX: (650) 845-4166
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 348 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: BLADNOT04
;; CLONE: 1319265
US-09-071-709-2

Query Match 38.4%; Score 192.5; DB 4; Length 348;
Best Local Similarity 44.0%; Pred. No. 3.4e-15;
Matches 37; Conservative 11; Mismatches 31; Indels 5; Gaps 2;
QY 5 RSHDFCLVSKVVG-RCRASMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKKAT 63
DB 62 KOTEDYCLASNKVGRRCRGSFPRWYDPTQICKSFYGGCLGNKNYLRREECILACRG 121
QY 64 VTENATGDLATSRNAADSSVPSAP 87
DB 122 V----QGGPLRGSSGAQATFPQGP 141

RESULT 8
US-08-358-160-71
; Sequence 71, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/358,160
;; FILING DATE: 16-DEC-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/133,031
;; FILING DATE: 13-OCT-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/009,319
;; FILING DATE: 26-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/664,989
;; FILING DATE: 01-MAR-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/487,063
;; FILING DATE: 02-MAR-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/240,160
;; FILING DATE: 02-SEP-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cooper, Iver P.
;; REGISTRATION NUMBER: 28,005
;; REFERENCE/DOCKET NUMBER: LEY=1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;; INFORMATION FOR SEQ ID NO: 71:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 58 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-358-160-71
Query Match 35.9%; Score 180; DB 1; Length 58;
Best Local Similarity 52.8%; Pred. No. 1.2e-14;
Matches 28; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
QY 9 DFCLYKVVYGRASMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 61
DB 3 DFCLLPATGTGPRAMPREFYNNAKSKCEPFYGGCGGNANFKTEECRRTC 55
RESULT 9
US-08-676-124-93
; Sequence 93, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,124

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-414-878-93

Query Match 34.7%; Score 174; DB 3; Length 58;
Best Local Similarity 49.1%; Pred. No. 6.1e-14;
Matches 27; Conservative 9; Mismatches 19; Indels 0;

QY 7 IHDFCLVSVGVGRASMPRWYNYVTDGSCQLFVYGGDGNSSNNYITKECLKKC 61
DB 1 MHSFCAKFAEYVGRASFPFRWFNFITRQCEFIYGGCEGNGNRFSELECKKMC 55

RESULT 11
US-09-240-136-93
; Sequence 93, Application US/09240136
; Patent No. 6103499
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,136
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994

```

ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-136-93

Query Match 34.7%; Score 174; DB 3; Length 58;
Best Local Similarity 49.1%; Pred. No. 6.1e-14;
Matches 27; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 7 IHDFCLVSKVGRCRASPRWYNYVDGSCQLFVYGGCDGNSNNYLTKEECLKKC 61
DB 1 MHSFCAKAEVGPGRASFPWFNFTQCEBFYVGGCEGNQNFESLECKKMC 55

RESULT 12

US-08-358-160-97
Sequence 97, Application US/08358160
Patent No. 5663143

GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-97

Query Match 33.3%; Score 167; DB 1; Length 62;
Best Local Similarity 52.7%; Pred. No. 4.5e-13;
Matches 29; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 7 IHDFCLVSKVGRCRASPRWYNYVDGSCQLFVYGGCDGNSNNYLTKEECLKKC 61
DB 1 INGDCPLKVGPCRARFPYYNSSSKRCKRPFYGGCGGNANFHTLEECRVC 55

RESULT 13

US-08-676-124-126
Sequence 126, Application US/08676124
Patent No. 6010880

GENERAL INFORMATION:
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert Charles
TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,124
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,658
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,265
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: MARKLAND-3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 13:16:05 ; Search time 16.15 Seconds
(without alignments)
547.382 Million cell updates/sec

Title: US-09-218-913D-8
Perfect score: 501
Sequence: 1 ADERSIHDFCLVSKVGRG.....ATSRNAADSSVPSAPRRQDS 92

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	360	71.9	252	2 JG0185	hepatocyte growth
2	167	33.3	62	2 S07451	proteinase inhibit
3	159	31.7	100	2 A32282	Alzheimer's diseas
4	159	31.7	265	2 A53390	Kunitz-type protei
5	157.5	31.4	765	2 S42880	amyloid precursor-
6	156.5	31.2	484	4 A32761	hypothetical Alzhe
7	156	31.1	64	2 S41399	Kunitz-type protei
8	155.5	31.0	302	1 T1RTGK	tissue factor path
9	155.5	31.0	751	2 A49974	beta-amyloid precu
10	155	30.9	60	1 T1BOR	serum basic protei
11	155	30.9	76	2 S03607	Alzheimer's diseas
12	155	30.9	100	1 T1BOSP	spleen basic prote
13	155	30.9	747	2 QH0773	Alzheimer's diseas
14	155	30.9	770	1 QH0773	Alzheimer's diseas
15	154	30.7	59	2 S00371	isoaprotinin G1 -
16	154	30.7	111	2 S41082	amyloid precursor
17	154	30.7	299	2 I46937	tissue factor path
18	153	30.5	76	2 S04855	Alzheimer's diseas
19	153	30.5	76	2 S06678	Alzheimer's diseas
20	152.5	30.5	300	2 S12143	lipoprotein-associ
21	152.5	30.4	763	2 A49321	amyloid beta (A4)
22	152	30.3	65	1 T1V1VC	venom basic protei
23	150.5	30.0	60	1 T1VRV2	venom basic protei
24	150.5	30.0	122	1 A55115	uterine plasmin/tr
25	150	29.9	110	1 T1T1OR	basic proteinase i
26	150	29.9	396	2 S53325	tissue factor path
27	149	29.7	58	2 S10063	isoaprotinin G2 -
28	149	29.7	61	1 T1V1T1	venom basic protei
29	147	29.3	67	1 T1B0C	trypsin inhibitor,

ALIGNMENTS

RESULT 1

JG0185

hepatocyte growth factor activator inhibitor type 2 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000

C:Accession: JG0185

R:Itoh, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Kono, M.

Biochem. Biophys. Res. Commun. 255, 740-748, 1999

A:Title: Hepatocyte growth factor activator inhibitor type 2 lacking the first kunitz,

A:Reference number: JG0185; MUID:99160423

A:Accession: JG0185

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-252 <ITO>

A:Cross-references: GB:AF099016

C:Superfamily: animal Kunitz-type proteinase inhibitor homology

F:133-183/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 71.9%; Score 360; DB 2; Length 252;
Best Local Similarity 69.6%; Pred. No. 3.6e-31;
Matches 64; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ADERSIHDFCLVSKVGRGCRASMPRWYNTYDSCQLFVYGGCDGNSNYLTKECLKK 60

Db 28 ASRELDVHESGVSKVCKRASIPRWYNTYDSCQFPVYGGCGNGNNTYQSKEECLDK 87

Oy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92

Db 88 CAGVTENTDDNARNRGADSSVLSVPRKQSA 119

RESULT 2

S07451

proteinase inhibitor 5.II - snake-locks sea anemone

C:Species: Anemonia sulcata (snake-locks sea anemone)

C>Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-May-1997

C:Accession: S07451; B27222

R:Wunderer, G.; Machleidt, W.; Fritz, H.

Meth. Enzymol. 80, 816-820, 1981

A:Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemoni

A:Reference number: S07451

A:Accession: S07451

A:Molecule type: protein

A:Residues: 1-59 <WUN>

A>Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found

R:Krebs, H.C.; Habermehl, G.G.

Naturwissenschaften 74, 395-396, 1987

A:Title: Isolierung und strukturaufklaerung eines haemolytisch aktiven peptids aus de

A:Reference number: A94700

A:Accession: B27222

A:Molecule type: protein

Db 340 VIP-----ATAASTPDA 351

RESULT 14

ORHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibitor
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
 C:Accession: S02260; S05194; A32277; A33860; A39486; I39452; I39451; I39453; I59562; A44
 4668; A28583; A29302; A60803; J06121; A60355; A59011; A38384; S29076; S38252; S3
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:89128427
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288,'V',365-770 <LEM1>
 A:Cross-references: EMBL:X13466
 A:Note: alternative splice form APP(695)
 R:Lemaire, H.G.
 submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
 A:Note: alternative splice form APP(695)
 R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
 A:Reference number: A32277; MUID:89165870
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LA>
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
 A:Reference number: A33260; MUID:89392030
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
 R:Prelli, F.; Levy, E.; van Dulmen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE>
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318
 A:Accession: I39452
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M33112; NID:g178613; PIDN:AA59502.1; PID:g178616
 A:Accession: I39451
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
 A:Molecule type: DNA
 A:Residues: 1-530,'QWLMVPVAFWEAKVGR' <YOS2>
 A:Cross-references: GB:M34875; NID:g178608; PIDN:AA59501.1; PID:g178615
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference I39451

R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo
 A:Reference number: I39453; MUID:90260663
 A:Accession: I39453
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
 A:Reference number: I59562; MUID:92022553
 A:Accession: I59562
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716,'F',718-737 <MUR>
 A:Cross-references: GB:S57665; NID:g236720; PIDN:AA819991.1; PID:g236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t
 A:Reference number: A44017; MUID:93035397
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692,'G',694-718 <KAM1>
 A:Cross-references: GB:S45135; NID:g257377; PIDN:AA823645.1; PID:g257378
 A:Experimental source: familial Alzheimer disease family SB
 A:Note: sequence extracted from NCBI backbone (NCBIP:II15374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>
 A:Cross-references: GB:S45136; NID:g257379; PIDN:AA823646.1; PID:g257380
 A:Experimental source: familial Alzheimer disease family LIT
 A:Note: this sequence has a silent mutation
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.
 Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-sur
 A:Reference number: A03134; MUID:87144572
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288,'V',365-770 <KAN>
 A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
 A:Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288,'V',365-646,'E',648-770 <ROB>
 A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
 A:Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amylo
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756,'S',758-770 <GOL>
 A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
 A:Experimental source: brain
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TANI>
 A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
 R:Dyrks, T.; Weidemann, A.; Multhaup, J.M.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue

Search completed: September 10, 2002, 13:18:18
Job time: 133 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2002, 13:17:56 ; Search time 11.86 seconds
(without alignments)
300.354 Million cell updates/sec

Title: US-09-218-913D-8

Perfect score: 501

Sequence: 1 ADRESIHDFCLVSKVVGRC.....ATSRNAADSSVPSAPRRQDS 92

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	501	100.0	252	1 SPT2_HUMAN	O43291 homo sapien
2	365	72.9	252	1 SPT2_MOUSE	Q9wu03 mus musculu
3	197	39.3	513	1 SPT1_HUMAN	O43278 homo sapien
4	181	36.1	507	1 SPT1_MOUSE	Q9r097 mus musculu
5	175.5	35.0	69	1 CRPT_BOOMI	P81162 boophilus m
6	170	33.9	58	1 AXPL_ANTAF	P81547 anthopleura
7	167	33.3	62	1 IP52_ANESU	P10280 anemonia su
8	166.5	33.2	306	1 TPPI_MOUSE	O54819 mus musculu
9	161	32.1	770	1 A4_RAT	P08592 rattus norv
10	160.5	32.0	751	1 A4_SAISC	Q95241 salmimi sci
11	159	31.7	133	1 EPPI_HUMAN	O95925 homo sapien
12	159	31.7	265	1 TKD1_SHEEP	Q29428 oviv aries
13	159	31.7	770	1 A4_MOUSE	P12023 mus musculu
14	157.5	31.4	765	1 APP2_RAT	P15943 rattus norv
15	156	31.1	64	1 SPT3_HUMAN	P49223 homo sapien
16	156	31.1	87	1 A4_MACFA	P53601 macaca fasc
17	156	31.1	164	1 TKD1_BOVIN	Q28201 bos taurus
18	156	31.1	197	1 MCPI_MELCP	P82968 melithaea c
19	155.5	31.0	302	1 TPPI_RAT	Q02445 rattus norv
20	155	30.9	60	1 IBPS_BOVIN	P00975 bos taurus
21	155	30.9	100	1 BP2_BOVIN	P04815 bos taurus
22	155	30.9	770	1 A4_HUMAN	P05067 homo sapien
23	154	30.7	300	1 TPPI_RABIT	P19761 oryctolagus
24	153	30.5	76	1 A4_MACMU	P29216 macaca mula
25	152.5	30.4	763	1 APP2_HUMAN	Q06481 homo sapien
26	152	30.3	65	1 IVB3_VIPAA	P00992 vipera amno
27	152	30.3	134	1 EPPI_MOUSE	Q9da01 mus musculu
28	150.5	30.0	60	1 IVB2_DABRU	P00990 dabovia russ
29	150.5	30.0	122	1 UPT1_PIG	Q29100 sus scrofa
30	150	30.0	110	1 IBP_CARCR	P00993 caretta car
31	149	29.7	61	1 IVB1_VIPAA	P00991 vipera amno
32	147	29.3	67	1 IBPC_BOVIN	P00976 bos taurus
33	147	29.3	100	1 BPT1_BOVIN	P00974 bos taurus

34	147	29.3	352	1 AMBP_HUMAN	P02760 homo sapien
35	146	29.1	304	1 TPPI_HUMAN	P10646 homo sapien
36	146	29.1	352	1 AMBP_BOVIN	P00978 bos taurus
37	145	28.9	55	1 ISH2_STOHE	P81129 stoichiactis
38	145	28.9	62	1 IVBT_ERINA	P24541 eristocophi
39	144	28.7	346	1 AMBP_MERUN	Q62577 meriones un
40	143	28.5	83	1 ELAC_MACEU	O62845 equus cabal
41	142	28.3	123	1 IATR_HORSE	P04365 equus cabal
42	142	28.3	133	1 EPPI_MACMU	Q9bd11 macaca mula
43	142	28.3	3137	1 CA36_CHICK	P15989 gallus gall
44	141	28.1	65	1 IVB1_BUNFA	P25660 bungarus fa
45	141	28.1	304	1 TPPI_MACMU	Q28864 macaca mula

ALIGNMENTS

RESULT 1
SPT2_HUMAN
ID SPT2_HUMAN STANDARD; PRT; 252 AA.
AC O43291; O00271; O14895; Q969E0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor activator inhibitor type 2) (HAI-2) (Placental bikunin).
GN SPINT2 OR HAI2 OR KOP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96010584; PubMed=9346890;
RA Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denda K., Kitamura N.;
RT "Purification and cloning of hepatocyte growth factor activator inhibitor type 2, a Kunitz-type serine protease inhibitor.";
RL J. Biol. Chem. 272:27558-27564(1997).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC TISSUE=Placenta;
RX MEDLINE=97277372; PubMed=9115294;
RA Marlor C.W., Delaria K.A., Davis G., Muller D.K., Greve J.M., Tamburini P.P.;
RT "Identification and cloning of human placental bikunin, a novel serine protease inhibitor containing two Kunitz domains.";
RL J. Biol. Chem. 272:12202-12208(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancratic cancer;
RX MEDLINE=98094245; PubMed=9434156;
RA Mueller-Pillasch F., Wallrapp C., Bartels K., Varga G., Friess H., Buechler M., Adler G., Gress T.M.;
RT "Cloning of a new Kunitz-type protease inhibitor with a putative transmembrane domain overexpressed in pancreatic cancer.";
RL Biochim. Biophys. Acta 1395:88-95(1998).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT LEU-200.
RC TISSUE=Colon, and Ovary;
RA Strausberg R.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN, PLASMA AND TISSUE KALLIKREIN, AND FACTOR XIA.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS, PROSTATE, TESTIS, THYMUS, AND TRACHEA.
CC -!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
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CC EMBL; AB006534; BAA35024.1; -
CC EMBL; U78095; AAC02781.1; -
CC EMBL; AF027205; AAB84031.1; -
CC EMBL; BC001668; AAH01668.1; -
CC EMBL; BC007705; AAH07705.1; -
CC EMBL; BC011951; AAH11951.1; -
CC EMBL; BC011955; AAH11955.1; -
CC EMBL; BC012868; AAH12868.1; -
CC HSSP; P05067; ITAM.
CC MIM; 605124; -
CC InterPro; IPR002223; Kunitz_BPTI.
CC Pfam; PF00014; Kunitz_BPTI; 2.
CC PRINTS; PR00759; BASICPTASE.
CC SMART; SM00131; KU; 2.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 2.
CC PROSITE; PS00279; BPTI_KUNITZ_2; 2.
KW Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;
KW Signal; Polymorphism
FT SIGNAL 1 27
FT CHAIN 28 252 KUNITZ-TYPE PROTEASE INHIBITOR 2.
FT DOMAIN 28 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 218 POTENTIAL.
FT DOMAIN 219 252 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 38 88 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 133 183 BPTI/KUNITZ INHIBITOR 2.
FT DISULFID 38 88 BY SIMILARITY.
FT DISULFID 47 71 BY SIMILARITY.
FT ACT_SITE 48 49 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 133 183 BY SIMILARITY.
FT DISULFID 142 166 BY SIMILARITY.
FT DISULFID 158 179 BY SIMILARITY.
FT ACT_SITE 143 144 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .).
FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 200 200 V -> L.
FT /FTID-VAR_012482.
FT CONFLICT 3 3 Q -> H (IN REF. 3).
FT CONFLICT 11 11 R -> P (IN REF. 1).
FT CONFLICT 53 53 R -> K (IN REF. 3).
FT CONFLICT 240 240 D -> H (IN REF. 3).
SQ SEQUENCE 252 AA; 28228 MW; A7D3360C0EECAB2B CRC64;

Query Match 100.0%; Score 501; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 2.2e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVGVGCRASMPRWYNTVDGSCQLFVYGGCDGNSNNYLTKECLKK 60
DB 28 ADERSIHDFCLVSKVGVGCRASMPRWYNTVDGSCQLFVYGGCDGNSNNYLTKECLKK 87
QY 61 CATVTENATGDLATSNRAADSSVSPAPRRQDS 92
DB 88 CATVTENATGDLATSNRAADSSVSPAPRRQDS 119

RESULT 2
SPT2_MOUSE STANDARD; PRT; 252 AA.
AC Q9WU03; Q9WU04; Q9WU05;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor
DE activator inhibitor type 2) (HAI-2).
GN SPINT2 OR HAI2.
OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=BALE/C;
RX MEDLINE=99160423; PubMed=10049781;
RA Itoh H., Kataoka H., Hamasuna R., Kitamura N., Koono M.;
RT "Hepatocyte growth factor activator inhibitor type 2 lacking the first
RT Kunitz-type serine proteinase inhibitor domain is a predominant
RT product in mouse but not in human.";
RL Biochem. Biophys. Res. Commun. 255:740-748(1999).
CC -!- FUNCTION: INHIBITOR OF HGF ACTIVATOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: ISOFORM 2 IS MORE PREDOMINANTLY EXPRESSED THAN
CC ISOFORM 1.
CC -!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).

CC EMBL; AF099016; AAD22172.1; -
CC EMBL; AF099019; AAD22173.1; -
CC EMBL; AF099020; AAD22174.1; -
CC HSSP; P05067; ITAM.
CC MGD; MGI:1338031; Splint2.
CC InterPro; IPR002223; Kunitz_BPTI.
CC Pfam; PF00014; Kunitz_BPTI; 2.
CC PRINTS; PR00759; BASICPTASE.
CC SMART; SM00131; KU; 2.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 2.
CC PROSITE; PS00279; BPTI_KUNITZ_2; 2.
KW Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;
KW Signal; Alternative splicing. POTENTIAL.
FT SIGNAL 1 27
FT CHAIN 28 252 KUNITZ-TYPE PROTEASE INHIBITOR 2.
FT DOMAIN 28 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 218 POTENTIAL.
FT DOMAIN 219 252 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 38 88 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 133 183 BPTI/KUNITZ INHIBITOR 2.
FT DISULFID 38 88 BY SIMILARITY.
FT DISULFID 47 71 BY SIMILARITY.
FT DISULFID 63 84 BY SIMILARITY.
FT ACT_SITE 48 49 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 133 183 BY SIMILARITY.
FT DISULFID 142 166 BY SIMILARITY.
FT DISULFID 158 179 BY SIMILARITY.
FT ACT_SITE 143 144 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 37 93 MISSING (IN ISOFORM 2 AND ISOFORM 3).
FT VARSPLIC 114 128 PRKQSAEDLSAEIFN -> CFVELSVAALFEYA (IN
FT ISOFORM 3).
FT VARSPLIC 129 252 MISSING (IN ISOFORM 3).
SQ SEQUENCE 252 AA; 27914 MW; B2FF4B86924D4F8F CRC64;

Query Match 72.9%; Score 365; DB 1; Length 252;
Best Local Similarity 69.6%; Pred. No. 2.6e-33;
Matches 64; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVGVGCRASMPRWYNTVDGSCQLFVYGGCDGNSNNYLTKECLKK 60
DB 28 ASRELDVHESCGVSKVGVGCRASIPRWYNTDGSQCFVYGGCEGNGNYSKECLDK 87

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Qy 61 CATVTENATGLATSRNADSSVSPAPRRQDS 92
    II IIII I : I : II IIII I II : I :
Db 88 CAGVTENTDDMRNRNGADSSVLSVPRKQSA 119
    II IIII I : I : II IIII I II : I :

RESULT 3
SPT1_HUMAN
ID SPT1_HUMAN STANDARD; PRT; 513 AA.
AC 043278;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor
DE activator inhibitor type 1) (HAI-1).
GN SPINT1 OR HAI1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97197808; PubMed=9045658;
RA Shimomura T., Denda K., Kitamura A., Kawaguchi T., Kito M., Kondo J.,
RA Kagaya S., Qin L., Takata H., Miyazawa K., Kitamura N.;
RT "Hepatocyte growth factor activator inhibitor, a novel Kunitz-type
RT serine protease inhibitor.";
RL J. Biol. Chem. 272:6370-6376(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue-Colon;
RC Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC Tissue-Milk;
RX MEDLINE=99303582; PubMed=10373425;
RA Lin C.Y., Anders J., Johnson M., Dickson R.B.;
RT "Purification and characterization of a complex containing matrilptase
RT and a Kunitz-type serine protease inhibitor from human milk.";
RL J. Biol. Chem. 274:18237-18242(1999).
CC -1- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO ACTS AS AN INHIBITOR OF
CC MATRIPTASE (ST1A).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
CC
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CC
CC EMBL; AB000095; BAA25014.1; -.
CC EMBL; BC004140; AAH04140.1; -.
CC HSSP; P31713; 1SHP.
CC MIM; 605123; -.
CC InterPro; IPR002223; Kunitz_BPTI.
CC InterPro; IPR002172; LDL_recept_A.
CC Pfam; PF00014; Kunitz_BPTI; 2.
CC Pfam; PF00057; ldl_recept_a; 1.
CC PRINTS; PR00759; BASICPTASE.
CC SMART; SM00131; KU; 2.
CC SMART; SM00192; LDLA; 1.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 2.
CC PROSITE; PS02079; BPTI_KUNITZ_2; 2.
CC PROSITE; PS01209; LDLRA_1; 1.
CC PROSITE; PS00068; LDLRA_2; 1.
KW Serine protease inhibitor; Repeat; Glycoprotein; Signal.
FT SIGNAL 1 35

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FT CHAIN 36 513 KUNITZ-TYPE PROTEASE INHIBITOR 1.
FT DOMAIN 250 300 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 318 354 LDL-RECEPTOR CLASS A.
FT DOMAIN 375 425 BPTI/KUNITZ INHIBITOR 2.
FT DISULFID 250 300 BY SIMILARITY.
FT DISULFID 259 283 BY SIMILARITY.
FT DISULFID 275 296 BY SIMILARITY.
FT ACT_SITE 260 261 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 375 425 BY SIMILARITY.
FT DISULFID 384 408 BY SIMILARITY.
FT DISULFID 400 421 BY SIMILARITY.
FT ACT_SITE 385 386 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 513 AA; 56885 MW; D6E05F3A5885CDDD CRC64;

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Query Match 39.3%; Score 197; DB 1; Length 513;
Best Local Similarity 55.0%; Pred. No. 2.3e-14;
Matches 33; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 5 RSIHDFCLVSKVGRCRASMPRWNVTDGSCQLFVYGGCDGNSNNYLTKBECLKKCATV 64
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 KQTEDYCLASNKVGRGSGFRWYDPTQICKSFYGGCLGNKNYLREECILACRGV 303
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
SPT1_MOUSE
ID SPT1_MOUSE STANDARD; PRT; 507 AA.
AC Q9R097;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor
DE activator inhibitor type 1) (HAI-1).
GN SPINT1 OR HAI1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Itoh H., Kataoka H., Koono H.;
RT "Mouse hepatocyte growth factor activator inhibitor type 1 (HAI-1).";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITOR OF HGF ACTIVATOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF099018; AAF02490.1; -.
CC HSSP; P05067; 1TAW.
CC MGD; MGI:1338033; Spintl.
CC InterPro; IPR002223; Kunitz_BPTI.
CC InterPro; IPR002172; LDL_recept_A.
CC Pfam; PF00014; Kunitz_BPTI; 2.
CC Pfam; PF00057; ldl_recept_a; 1.
CC PRINTS; PR00759; BASICPTASE.
CC SMART; SM00131; KU; 2.
CC SMART; SM00192; LDLA; 1.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 2.
CC PROSITE; PS02079; BPTI_KUNITZ_2; 2.

```

```
DR PROSITE; PS01209; LDLRA_1; FALSE_NEG.
KW Serine protease inhibitor; Repeat; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 507
FT DOMAIN 244 294
FT DOMAIN 312 348
FT DOMAIN 369 419
FT DISULFID 244 294
FT DISULFID 253 277
FT DISULFID 269 290
FT ACT_SITE 254 255
FT DISULFID 369 419
FT DISULFID 378 402
FT DISULFID 394 415
FT ACT_SITE 379 380
FT CARBOHYD 229 229
FT CARBOHYD 501 501
SQ SEQUENCE 507 AA; 56676 MW; 20CB5DEDCFE46AA7 CRC64;

Query Match 36.1%; Score 181; DB 1; Length 507;
Best Local Similarity 53.6%; Pred. No. 1.3e-12;
Matches 30; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

* QY 9 DFLVSKVVGRCRASPRWVNYVDGSCQLFVYGGDGNNSNNYLTKKECLKKCATV 64
Db 242 DYCLASYKVGRCGSPRWYDPKQICKSFTEGGCLGNKNYLREECMLACKDV 297

- RESULT 5
CRPT_BOOMI
ID CRPT_BOOMI STANDARD; PRT; 69 AA.
AC P81162;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protease inhibitor carrapatin.
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE.
RA Fuentes-Prior P., Pereira P.J.B., Mentale R., Bode W.;
RL Submitted (JAN-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: SERINE-PROTEASE INHIBITOR.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
DR HSP; P10646; ITEX.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 8 58
FT DISULFID 17 41
FT DISULFID 33 54
FT ACT_SITE 18 19
SQ SEQUENCE 69 AA; 7842 MW; E0B14312AC1533BB CRC64;

Query Match 35.0%; Score 175.5; DB 1; Length 69;
Best Local Similarity 47.8%; Pred. No. 6.3e-13;
Matches 32; Conservative 8; Mismatches 22; Indels 5; Gaps 2;

QY 9 DFLVSKVVGRCRASPRWVNYVDGSCQLFVYGGDGNNSNNYLTKKECLKKCATV 65
Db 3 DFDKQCVPTADPGCKGFMPWVNYIFTSQCEEFYVGGQNDNRYRTKECDKTCAEA- 61
QY 66 ENATGDL 72
Db 62 -SATWDV 67
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RESULT 6

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AXPL_ANTAF
ID AXPL_ANTAF STANDARD; PRT; 58 AA.
AC P81547;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kunitz-type proteinase inhibitor AXPI-I.
DE Anthopleura aff. xanthogrammica (Sea anemone).
OS Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actinidae; Anthopleura.
OX NCBI_TaxID=152178;
RN [1]
RP SEQUENCE.
RX MEDLINE=98103405; PubMed=9440231;
RA Minagawa S., Ishida M., Shimakura K., Nagashima Y., Shiomi K.;
RT "Isolation and amino acid sequences of two kunitz-type protease
inhibitors from the sea anemone Anthopleura aff. xanthogrammica.";
RL Comp. Biochem. Physiol. 118B:381-386(1997).
CC -!- FUNCTION: SPECIFIC FOR SERINE PROTEASES, ESPECIALLY TRYPSIN. ALSO
WEAK INHIBITION AGAINST ALPHA-CHYMOTRYPSIN, ELASTASE AND SOME
METALLOPROTEASES.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 7 57
FT DISULFID 16 40
FT DISULFID 32 53
FT ACT_SITE 17 18
SQ SEQUENCE 58 AA; 6341 MW; DA27216A535EA7CC CRC64;
```

Query Match 33.9%; Score 170; DB 1; Length 58;
Best Local Similarity 49.1%; Pred. No. 2.1e-12;
Matches 27; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

```
QY 7 IHDFCLVSKVVGRCRASPRWVNYVDGSCQLFVYGGDGNNSNNYLTKKECLKK 61
Db 3 VNEDCLLPKVGPCRAAVPRFYNSDSGRCEGTYGGCHANANFKDKDECKNAC 57
```

RESULT 7

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IP52_ANESU
ID IP52_ANESU STANDARD; PRT; 62 AA.
AC P10280;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protease inhibitor 5 II (SA5 II).
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actinidae; Anemonia.
OX NCBI_TaxID=6108;
RN [1]
RP SEQUENCE OF 1-59.
RA Wunderer G., Machleidt W., Fritz H.;
RT "The broad-specificity proteinase inhibitor 5 II from the sea anemone
Anemonia sulcata.";
RL Meth. Enzymol. 80:816-820(1981).
RN [2]
RP SEQUENCE.
RA Krebs H.C., Habermehl G.G.;
RT "Isolation and structural determination of a hemolytic active peptide
from the sea anemone Metridium senile.";
RL Naturwissenschaften 74:395-396(1987).
CC -!- FUNCTION: INHIBITOR OF KALLIKREINS.
```

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CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
DR PIR: B27222; B27222.
DR PIR: S07451; S07451.
DR HSP: P10646; 1TFX.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT_SITE 15 16 REACTIVE BOND (BY SIMILARITY).
FT VARIANT 13 13 P -> R.
FT VARIANT 16 16 A -> G.
FT VARIANT 17 17 R -> G.
FT VARIANT 25 25 S -> L.
FT VARIANT 28 28 K -> R.
FT VARIANT 39 39 G -> R.
SQ SEQUENCE 62 AA; 6937 MW; 7262D028CA567BC8 CRC64;

Query Match 33.3%; Score 167; DB 1; Length 62;
Best Local Similarity 52.7%; Pred. No. 4.9e-12;
Matches 29; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 7 IHDFCLSVKVGRCRSMRWYNTDSCQLFYVGGCDGNSNNYLTKECLKKC 61
Db 1 INGDELPKVVGPCRPRFYNNSSSKRCCKFYGGCGGNANFHTLECEKVC 55

RESULT 8
TFPI_MOUSE
ID TFPI_MOUSE STANDARD; PRT; 306 AA.
AC 054819; Q92208;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
DE associated coagulation inhibitor) (LACI) (extrinsic pathway inhibitor)
DE (EPI).
GN TFPI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A. (ISOFORM ALPHA).
RP STRAIN=129;
RX MEDLINE=98152575; PubMed=9493581;
RA Chang J.-Y., Monroe D.M., Oliver J.A., Liles D.K., Roberts H.R.;
RT "Cloning, expression, and characterization of mouse tissue factor
RT pathway inhibitor (TFPI).";
RL Thromb. Haemost. 79:306-309(1998).
[2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX MEDLINE=99138770; PubMed=9974373;
RA Chang J.-Y., Monroe D.M., Oliver J.A., Roberts H.R.;
RT "TFPIbeta, a second product from the mouse tissue factor pathway
RT inhibitor (TFPI) gene.";
RL Thromb. Haemost. 81:45-49(1999).
CC -1- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
CC ANTI-THROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
CC LIPOPROTEINS IN PLASMA (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha/TFPIalpha (shown here) and
CC beta/TFPIbeta; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Isoform alpha is expressed in heart and
CC spleen; isoform beta in heart and lung.

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CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
CC
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CC
CC EMBL; AF004833; AAC40035.1; -.
CC EMBL; AF016313; AAD01586.1; -.
CC HSP: P10646; 1TFX.
CC MGD: MGI:1095418; Tfpi.
CC InterPro: IPR002223; Kunitz_BPTI.
CC Pfam: PF00014; Kunitz_BPTI; 3.
CC PRINTS: PR00759; BASICPTASE.
CC SMART: SM00131; KU; 3.
CC PROSITE: PS00280; BPTI_KUNITZ_1; 3.
CC PROSITE: PS0279; BPTI_KUNITZ_2; 3.
KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW Signal; Alternative splicing.
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 306 TISSUE FACTOR PATHWAY INHIBITOR.
FT DOMAIN 50 100 BPTI/KUNITZ INHIBITOR 1
(VII(A)/TISSUE FACTOR BINDING SITE).
FT DOMAIN 121 171 BPTI/KUNITZ INHIBITOR 2
(FACTOR X(A) BINDING SITE).
FT DOMAIN 225 275 BPTI/KUNITZ INHIBITOR 3.
FT DISULFID 50 100 BY SIMILARITY.
FT DISULFID 59 83 BY SIMILARITY.
FT DISULFID 75 96 BY SIMILARITY.
FT ACT_SITE 60 61 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 121 171 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 146 167 BY SIMILARITY.
FT ACT_SITE 131 132 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 225 275 BY SIMILARITY.
FT DISULFID 234 258 BY SIMILARITY.
FT ACT_SITE 235 236 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 254 254 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 264 264 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 282 282 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPPLIC 218 253 DYRGKPCWCLQADSLCKASRRFYNSATGCKHRF -> V
TKEETNGKKNADTYQGFLSSVYHLYFVFRIG (IN
ISOFORM BETA).
FT VARSPLIC 254 306 MISSING (IN ISOFORM BETA).
FT CONFLICT 68 F -> L (IN REF. 2).
SQ SEQUENCE 306 AA; 34987 MW; D3EA3297E4B6A359 CRC64;

Query Match 33.2%; Score 166.5; DB 1; Length 306;
Best Local Similarity 37.0%; Pred. No. 3.1e-11;
Matches 37; Conservative 9; Mismatches 37; Indels 17; Gaps 2;

QY 9 DFCLSVKVGRCRSMRWYNTDSCQLFYVGGCDGNSNNYLTKECLKKCAT----- 63
Db 119 DFCLEEDPGLCGYMKRYLYNNQTKQCFERFYVGGCLGNRNNFETLDECKKICENPVHSP 178
QY 64 -----VTE-NATGDLATSRNAADSSVPSAPRQD 91
Db 179 SPVNEVQMSDYVTGNTVTDRTVNNIVVQSPKVPVRRD 218

RESULT 9
A4_RAT
ID A4_RAT STANDARD; PRT; 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)

```

16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=89312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.;
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two, extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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CC -----
DR EMBL; X07648; CAA30488.1; -;
DR EMBL; X14066; CAA32229.1; -;
DR PIR; S00550; S00550.
DR PIR; S03607; S03607.
DR HSSP; P05067; IAAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT BY SIMILARITY.
FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT HOMOLOG.
FT DOMAIN 18 699
FT TRANSMEM 700 723
FT POTENTIAL.
FT DOMAIN 724 770
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 673 715
FT EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT DOMAIN 287 345
FT BPTI/KUNITZ INHIBITOR.
FT SITE 759 762
FT CLATHRIN-BINDING (BY SIMILARITY).
FT DISULFID 291 341

FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 E -> V (IN ISOFORM APP(695)).
FT VARSPLIC 290 MISSING (IN ISOFORM APP(695)).
SQ SEQUENCE 770 AA; 86704 MW; C26C9D6BB2D929A7 CRC64;

Query Match 32.1%; Score 161; DB 1; Length 770;
Best Local Similarity 40.0%; Pred. No. 3.4e-10;
Matches 26; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 4 ERSIHDFCLVWGRCRASPMWYNTVDGSCQLFVYGGCDGNSNYLTKECLKKCAT 63
DB 284 EEVREVCEQAETGFCRAMISRWFYDTEGKCAFFYGGCGGNRNFTTEYCMVCGS 343

QY 64 VTENA 68
DB 344 VSSQS 348

RESULT 10
A4_SAISC STANDARD; PRT; 751 AA.
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
DE amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Anorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
RT cerebral amyloid angiopathy.";
RL Neurobiol. Aging 16:805-808(1995).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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DR EMBL; S81024; AAD14347.1; -;
DR HSSP; P05067; IAAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.


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DR SMART: SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein: Amyloid; Neurone; Transmembrane; Alternative splicing;
KW Signal: Serine protease inhibitor.
FT SIGNAL 1
FT CHAIN 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND.
FT FT 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 32.0%; Score 160.5; DB 1; Length 751;
Best Local Similarity 37.7%; Pred. No. 3.8e-10;
Matches 29; Conservative 14; Mismatches 31; Indels 3; Gaps 1;

Oy 4 ERSIHDFCLVSKVWGRCRPMRWYNTDGSQCLFYVGGDGNSSNYLTKEECLKKCAT 63
Db 284 EKVREVCSQAEQPCRAMISRWTFDTEGKCAPFFYGGGGRNNDTEYCMVAVCS 343
Oy 64 VTENATGDLTSRNAAD 80
Db 344 VIPTTA---ASTPDAVD 357

RESULT 11
EPPI_HUMAN
ID EPPI_HUMAN STANDARD; PRT; 133 AA.
AC O95925; O9HD30; O96SD7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 06-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE EpPin precursor (Epilidymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN SPINLMI
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE-Epididymis, and Testis;
RX PubMed=11404006;
RA Richardson R.T., Sivashanmugam P., Hall S.H., Hamil K.G., Moore P.A.,
RA Ruben S.M., French P.S., O'Rand M.G.;
RA "Cloning and sequencing of human EpPin: a novel family of protease
RA inhibitors expressed in the epididymis and testis.";
RL Gene 270:93-102(2001).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP Stavrides G.S., Huckle E.J., Deloukas P.;
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R., Corby N.R.,

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RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall P.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivasalho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurray A.A.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
CC -!- PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN EPIDIDYMIS AND TESTIS.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
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EMBL; AF286370; AAG00548.1; -
EMBL; AF286369; AAG00547.1; -
EMBL; AF286368; AAG00546.1; -
EMBL; AL118493; CAB56343.1; -
EMBL; AL031663; CAB37635.1; -
EMBL; AL031663; CAB36265.1; -
HSSP; P00974; 2KAI.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00014; Kunitz_Bpti; 1.
DR Pfam; PF00095; wap; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal; Alternative splicing.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 133 EPPIN.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/KUNITZ INHIBITOR.
FT DISULFID 33 61 BY SIMILARITY.
FT DISULFID 40 65 BY SIMILARITY.
FT DISULFID 48 60 BY SIMILARITY.
FT DISULFID 54 69 BY SIMILARITY.
FT DISULFID 77 127 BY SIMILARITY.
FT DISULFID 86 110 BY SIMILARITY.
FT DISULFID 102 123 BY SIMILARITY.
FT VARSPIC 1 31 MGSSGLLSLVFLVLLANVQSGPLTDWLFPR -> MLSKAH
FT GCKTALSUG (IN ISOFORM 2).
SQ SEQUENCE 133 AA; 15284 MW; F7831B203366D9DC CRC64;

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Query Match 31.7%; Score 159; DB 1; Length 133;
 Best Local Similarity 47.2%; Pred. No. 8.6e-11;
 Matches 25; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

	QY	4	ERSIHDFCLVSKVVGRCSRASMPRWNTVDGSCQLFVYGCGDGNSSNNYTKEECLKKCAT	63
		:	: : :	
	Db	284	EENVREVCSEQAETGPCRAMISWIFYEDVTGCKVPFFYGGCGNRRNFDETYCMAVGS	343
	QY	64	VT	65
		:	:	
	Db	344	VS	345

FT	DISULFID	321	BY SIMILARITY.	345
FT	DISULFID	337	BY SIMILARITY.	358

```
FT DOMAIN 218 229 POLY-GLU.
FT CARBOHYD 628 628 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT VARSPLIC 311 365 MISSING (IN ISOFORM C AND ISOFORM D).
FT VARSPLIC 616 627 MISSING (IN ISOFORM B AND ISOFORM D).
FT CONFLICT 575 577 DOF -> EFV (IN REF. 2).
SQ SEQUENCE 765 AA; 86882 MW; CP51FCCCE305A0CF CRC64;

Query Match 31.4%; Score 157.5; DB 1; Length 765;
Best Local Similarity 38.5%; Pred. No. 8.3e-10;
Matches 30; Conservative 17; Mismatches 24; Indels 7; Gaps 3;

Oy 1 ADRESIHID---FCLVSKVVGCRASMPRWYNYVDGSCQLFVYGGCDGNSNNYLTKEEC 57
Db 300 SKETA-HDKAVCSQEAQPCRAVMPRWYFDLSKSKVRFYGGCGGNRRNFESEYDC 358

Oy 58 LKKCATV---TENAGDL 72
Db 359 MAVCKTMIPPTPLPTNDV 376

RESULT 15
SPT3_HUMAN
ID SPT3_HUMAN STANDARD; PRT; 64 AA.
AC P49223; Q96KK2;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Kunitz-type protease inhibitor 3 (HKIB9) (Fragment).
GN SPINT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=Placenta, and Blood;
RA Norris F., Norris K., Bjoern S.E., Petersen L.C., Foster D.C.,
RA Sprecher C.A.;
RA "A novel human Kunitz-type protease inhibitor and variants thereof.";
RL patent number WO9314123, 22-JUL-1993.
RN [2]
RP SEQUENCE OF 2-64 FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levaslatko M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RA "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: CONTAINS 1 BPPI/KUNITZ INHIBITOR DOMAIN.
CC
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DR EMBL; X77166; CAA54410.1; -.
DR EMBL; AL031663; CAB37639.1; -.
DR HSSP; P05067; 1TAW.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT NON_TER 1 1
FT DOMAIN 11 61 BPTI/KUNITZ INHIBITOR.
FT DISULFID 11 61 BY SIMILARITY.
FT DISULFID 20 44 BY SIMILARITY.
FT DISULFID 36 57 BY SIMILARITY.
FT ACT_SITE 21 22 REACTIVE BOND (BY SIMILARITY).
SQ SEQUENCE 64 AA; 7407 MW; 1DA1DDEDD9C86C7 CRC64;

Query Match 31.1%; Score 156; DB 1; Length 64;
Best Local Similarity 51.0%; Pred. No. 8.4e-11;
Matches 26; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Oy 11 CLVSKVVGCRASMPRWYNYVDGSCQLFVYGGCDGNSNNYLTKECLKKC 61
Db 11 CAFPMKPGCQTYMTRWFNFETGCELFAYGGCGGNSNFLRKEKCEKFC 61
```

Search completed: September 10, 2002, 13:21:45
Job time: 229 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 13:17:41 ; Search time 25.51 Seconds
(without alignments)
623.894 Million cell updates/sec

Title: US-09-218-913D-8

Perfect score: 501

Sequence: 1 ADERSIHDFCLVSKVVGRC.....ATSRNAADSSVPSAPRRQDS 92

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:**

- 1: sp_archaea:**
- 2: sp_bacteria:**
- 3: sp_fungi:**
- 4: sp_human:**
- 5: sp_invertebrate:**
- 6: sp_mammal:**
- 7: sp_mhc:**
- 8: sp_organelle:**
- 9: sp_phase:**
- 10: sp_plant:**
- 11: sp_rodent:**
- 12: sp_virus:**
- 13: sp_vertebrate:**
- 14: sp_unclassified:**
- 15: sp_rvirus:**
- 16: sp_bacteriap:**
- 17: sp_archaea:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	100.0	252	4	Q969E0
2	182	36.3	507	11	Q9D3K4
3	182	36.3	507	11	Q99J04
4	181.5	36.2	984	5	Q9GQK2
5	181.5	36.2	984	5	Q9GQK1
6	177	35.3	59	5	Q9TFP8
7	173	34.5	58	5	Q9TFP9
8	170	33.9	58	5	Q9TFG0
9	170	33.9	195	11	Q9D8Q8
10	169	33.7	154	6	Q9N0X3
11	169	33.7	183	6	Q9N0X5
12	161	32.1	83	13	Q90WA1
13	160.5	32.0	246	11	Q9Z2U8
14	159	31.7	117	4	Q96SD7
15	159	31.7	607	11	Q99K32
16	159	31.7	770	6	Q9TU10

17	158	31.5	351	6	Q9N0X8
18	156.5	31.2	484	4	Q13793
19	156	31.1	63	4	Q13793
20	156	31.1	160	11	Q90278
21	156	31.1	174	6	Q9N0X2
22	155.5	31.0	132	5	Q9VQF9
23	155.5	31.0	751	11	Q60709
24	155.5	31.0	763	11	Q61482
25	155	30.9	547	4	Q13764
26	155	30.9	747	13	Q91963
27	154	30.7	110	6	Q9N0X4
28	153.5	30.6	3198	5	Q90868
29	152.5	30.4	523	4	Q14594
30	152	30.3	179	6	Q9N0X6
31	151.5	30.2	751	13	Q9DG37
32	151	30.1	83	13	Q90WA0
33	150.5	30.0	3060	5	Q9VAV4
34	150	29.9	137	6	Q9BDL0
35	150	29.9	396	6	Q28874
36	149	29.7	74	11	Q60495
37	148.5	29.6	738	13	Q90W28
38	148	29.5	83	13	Q90W99
39	148	29.5	83	13	Q90W98
40	148	29.5	780	13	Q73683
41	147	29.3	151	4	P78491
42	146	29.1	251	4	Q95103
43	145	28.9	113	5	Q9V508
44	144.5	28.8	2167	5	Q76840
45	144	28.7	169	6	Q9N0X7

ALIGNMENTS

RESULT 1

Q969E0 ID Q969E0 PRELIMINARY; PRT: 252 AA.
AC Q969E0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SERINE PROTEASE INHIBITOR, KUNITZ TYPE, 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY, AND ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY, AND ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY, AND ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012868; AAH12868.1; -
DR EMBL; BC007705; AAH07705.1; -
DR EMBL; BC011951; AAH11951.1; -
DR EMBL; BC011955; AAH11955.1; -
KW Protease.
SQ SEQUENCE 252 AA; 28242 MW; FDD3360C1F3A7057 CRC64;

Query Match 100.0%; Score 501; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 4.le-52;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ADERSIHDFCLVSKVVGRCRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 60
Db 28 ADERSIHDFCLVSKVVGRCRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 87
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
Db 88 CATVTENATGDLATSRNAADSSVPSAPRRQDS 119

RESULT 2
Q9D3K4 PRELIMINARY; PRT; 507 AA.
AC Q9D3K4:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SERINE PROTEASE INHIBITOR, KUNITZ TYPE 1.
GN SPINT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HEAD;
RX MEDLINE=21083660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavita T.,
RA Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017342; BAB30697.1; -.
DR HSSP; P05067; 1CA0.
DR MGD; MGI:1338033; Spint1.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002172; LDL_recept_A.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; ldl_recept_a; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLa; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS00068; LDLRA_2; 1.
DR GlycoProtein; Serine protease inhibitor.
SQ SEQUENCE 507 AA; 56571 MW; 9E0A29B7056D72D CRC64;

Query Match 36.3%; Score 182; DB 11; Length 507;
Best Local Similarity 50.0%; Pred. No. 1.8e-13;
Matches 30; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

QY 5 RSIHDFCLVSKVVGRCRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKKATV 64
Db 238 KOTEDYCLASYKVGRCGSFPRWYDPKEQICKSTFTFGCLGNKNNYLREECMLACKDV 297

RESULT 3
Q9GQNZ PRELIMINARY; PRT; 984 AA.
AC Q9GQNZ:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PEPTIDYLGLYCINE ALPHA-AMIDATING MONOOXYGENASE.
GN PAM.
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Hormathidae; Calliactis.
OX NCBI_TaxID=6114;
RN [1]
RP SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Gimmelikhuijzen C.J.P.;
RT "Cloning of peptide alpha-amidating enzymes in Calliactis parasitica.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221985; AAG44250.1; -.
DR HSSP; P12111; 1KNT.
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR000720; Pamonoxigenase.
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF01436; NHL; 4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00790; PAMONOXGNASE.

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DR SMART; SM00131; KU; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
DR MONOOXYGENASE; Serine protease inhibitor.
SQ SEQUENCE 984 AA; 110267 MW; 7AFE2D1B74B78EBC CRC64;

Query Match 36.2%; Score 181.5; DB 5; Length 984;
Best Local Similarity 36.7%; Pred. No. 4.4e-13;
Matches 33; Conservative 17; Mismatches 39; Indels 1; Gaps 1;

QY 2 DRESDHDFCLVSKVVGRCRASMPRWYVNTDGSQQLFVYGGCDGNSNNYLTKEECLKK 61
Db 721 DNKASFPFCMLEHDTGCPRAAMPWFYDFAKARCTRFYGGCGSNNENFASKRECEAK 780

QY 62 A-TVTENATGDLATSRNAADSSVPSAPRQ 90
Db 781 TQIVNSNKQKQKNSGHISEMTLNNLPSKQ 810

RESULT 5
Q9GQNI O9GQNI PRELIMINARY; PRT; 984 AA.
AC O9GQNI; 2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PEPTIDYLGLYCINE ALPHA-AMIDATING MONOOXYGENASE.
GN PAM.
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Hormathidae; Calliactis.
OX NCBI_TaxID=6114;
RN 1
RP SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Grimmelikhuijzen C.J.P.;
RT "Cloning of peptide alpha-amidating enzymes in Calliactis
parasitica."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221986; AAC44251.1;
DR HSP; P12111; 1KNT
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR000720; Pamonooxygenase.
DR Pfam; PF01082; Cu2_monooxygen.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF01436; NHL; 4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
KW Monooxygenase; Serine protease inhibitor.
SQ SEQUENCE 984 AA; 110266 MW; 4C24E4BCEB3B480D CRC64;

Query Match 36.2%; Score 181.5; DB 5; Length 984;
Best Local Similarity 36.7%; Pred. No. 4.4e-13;
Matches 33; Conservative 17; Mismatches 39; Indels 1; Gaps 1;

QY 2 DRESDHDFCLVSKVVGRCRASMPRWYVNTDGSQQLFVYGGCDGNSNNYLTKEECLKK 61
Db 721 DNKASFPFCMLEHDTGCPRAAMPWFYDFAKARCTRFYGGCGSNNENFASKRECEAK 780

QY 62 A-TVTENATGDLATSRNAADSSVPSAPRQ 90
Db 781 TQIVNSNKQKQKNSGHISEMTLNNLPSKQ 810

RESULT 6
Q9TWF8 O9TWF8 PRELIMINARY; PRT; 59 AA.
QY 7 IHDFCLVSKVVGRCRASMPRWYVNTDGSQQLFVYGGCDGNSNNYLTKEECLKK 61
Db 1 INGDELPKVVGRCRAPRPRYYNLSRRCEKFIYGGCGNANNPHTLEECEKVC 55

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AC Q9TWF8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE KALICUDINE 3, ASKC3.
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anemonia.
OX NCBI_TaxID=6108;
RN 1
RP SEQUENCE.
RX MEDLINE=96027617; PubMed=7559645;
RA Beress L., Lazdunski M.;
RT "Kalicudines and kaliseptine. Two different classes of sea anemone
toxins for voltage sensitive K+ channels."
RL J. Biol. Chem. 270:25121-25126(1995).
DR HSP; P31713; 1SHP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 59 AA; 6738 MW; 0C7695C3F394D4A5 CRC64;

Query Match 35.3%; Score 177; DB 5; Length 59;
Best Local Similarity 54.5%; Pred. No. 6.2e-14;
Matches 30; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 7 IHDFCLVSKVVGRCRASMPRWYVNTDGSQQLFVYGGCDGNSNNYLTKEECLKK 61
Db 1 INGDELPKVVGRCRAPRPRYYNLSRRCEKFIYGGCGNANNPHTLEECEKVC 55

RESULT 7
Q9TWF9 O9TWF9 PRELIMINARY; PRT; 58 AA.
AC Q9TWF9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE KALICUDINE 2, ASKC2.
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anemonia.
OX NCBI_TaxID=6108;
RN 1
RP SEQUENCE.
RX MEDLINE=96027617; PubMed=7559645;
RA Beress L., Lazdunski M.;
RT "Kalicudines and kaliseptine. Two different classes of sea anemone
toxins for voltage sensitive K+ channels."
RL J. Biol. Chem. 270:25121-25126(1995).
DR HSP; P12111; 2KNT.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 58 AA; 6778 MW; F102E71682F1A55C CRC64;

Query Match 34.5%; Score 173; DB 5; Length 58;
Best Local Similarity 52.7%; Pred. No. 1.8e-13;
Matches 29; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 7 IHDFCLVSKVVGRCRASMPRWYVNTDGSQQLFVYGGCDGNSNNYLTKEECLKK 61

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[illegible]

Query Match	32.1%	Score 161;	DB 13;	Length 83;
Best Local Similarity	48.1%	Pred. No. 7.6e-12;		
Matches	26;	Conservative	9;	Mismatches 19; Indels 0; Gaps 0;
QY	9	DFCLYSKVVGRASMPRWNYVDGSCQLFVYGGCDGNSNYLTKECLKKCA	62	
DB	29	DFCELPAADTGPCVRFPSPFYFNPDEKCKLEFIYGGCEGNANFTTKECESTCA	82	
RESULT 13				
Q9Z2U8		PRELIMINARY;	PRT;	246 AA.
AC	Q9Z2U8			
DT	01-MAY-1999	(TREMBlrel. 10, Created)		
DT	01-MAY-1999	(TREMBlrel. 10, Last sequence update)		
DT	01-DEC-2001	(TREMBlrel. 19, Last annotation update)		
DE	TFPIBETA (FRAGMENT).			
GN	TFPI OR TFPIBETA.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129;			
RA	Chang J.-Y., Monroe D.M., Roberts H.R.;			
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF016313; AAD01586.1; -			
DR	HSSP: P10646; 1TFX.			
DR	MGI: 1095418; Tfpi.			
DR	InterPro: IPR002223; Kunitz_BPTI.			
DR	Pfam: PF00014; Kunitz_BPTI; 2.			
DR	PRINTS; PR00759; BASICPTASE.			
DR	SMART; SM00131; KU; 2.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 2.			
DR	PROSITE; PS0279; BPTI_KUNITZ_2; 2.			
KW	Serine protease inhibitor.			
FT	NON_TER			
SQ	SEQUENCE 246 AA; 28003 MW; 4BEDC23E04F07B6 CRC64;			
Query Match	32.0%	Score 160.5;	DB 11;	Length 246;
Best Local Similarity	36.4%	Pred. No. 3e-11;		
Matches	36;	Conservative	9;	Mismatches 37; Indels 17; Gaps 2;
QY	9	DFCLYSKVVGRASMPRWNYVDGSCQLFVYGGCDGNSNYLTKECLKKCAT	63	
DB	112	DFCFLEEDPGLCRGMYKRYLNQTKQCFERFVYGGCLGRNNFTLDECKKICENPVHSP	171	
QY	64	-----VTE-NATGDLATSRNAADSSVPSAPRQ	90	
DB	172	SPVNEVQMSDYVTGNTVTRDSTRNNIVVPSQPKVPRRR	210	
RESULT 14				
Q96SD7		PRELIMINARY;	PRT;	117 AA.
AC	Q96SD7			
DT	01-DEC-2001	(TREMBlrel. 19, Created)		
DT	01-DEC-2001	(TREMBlrel. 19, Last sequence update)		
DT	01-DEC-2001	(TREMBlrel. 19, Last annotation update)		
DE	DJ461P7.2.2 (EPPIN-2 (WAP-TYPE (WHEY ACIDIC PROTEIN)			
DE	'FOUR-DISULFIDE CORE' DOMAIN AND A KUNITZ/BOVINE PANCREATIC TRYPsin			
DE	INHIBITOR DOMAIN PROTEIN)).			
GN	DJ461P7.2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

RA Clark L.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031663; CAC36265.1; -
SQ SEQUENCE 117 AA; 13485 MW; 96161FAB3CFEDB47 CRC64;

Query Match 31.7%; Score 159; DB 4; Length 117;
Best Local Similarity 47.2%; Pred. No. 1.9e-11;
Matches 25; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 9 DFCLVSKVVGRCRASPWWYNTDGSQCLFYVGGCGNSNNYLTKEECLKKC 61
Db 59 DVCEMPKETGCPCLAYFLHWWYDKDKNTCSMEFYVGGCGNNNNFQSKANCLNTC 111

RESULT 15

Q99K32 PRELIMINARY; PRT; 607 AA.
AC Q99K32;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
TISSUE;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005490; AAH05490.1; -
DR HSP; P05067; IAPP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF0014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein; Serine protease inhibitor.
FT NON_TER 1
SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 31.7%; Score 159; DB 11; Length 607;
Best Local Similarity 41.9%; Pred. No. 1.3e-10;
Matches 26; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

QY 4 ERSIHDCLVSKVVGRCRASPWWYNTDGSQCLFYVGGCGNSNNYLTKEECLKKCAT 63
Db 121 EEVVRVCSEQAETGCRAMISRWYFDVTEGKCVPPFYGGCGGNRNNFTDEYCMVAVCGS 180
QY 64 VT 65
Db 181 VS 182

Search completed: September 10, 2002, 13:21:27
Job time: 226 sec